REMARKS

Applicants add SEQ ID NOs to the specification and claims. Applicants believe the present replacement sequence disclosure discloses all sequences in the specification.

The content of the paper copy of the Sequence Listing and the copy of the Sequence Listing in computer readable form is the same, and includes no new matter.

Please charge any shortage in fees due in connection with the filing of this paper, including Extension of Time fees to Deposit Account No. 11-0345. Please credit any excess fees to such account.

Respectfully submitted,
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VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE SPECIFICATION

Amend the paragraph on page 14, lines 36 to 46 as follows:

The suitable sequences are selected by comparing with the binding affinity to the immobilized metal ions of the following natural Helicobacter pylori ATPase-439 sequence His-Ile-His-Asn-Leu-Asp-Cys-Pro-Asp-Cys (SEQ ID NO: 11). The protein fragment sequences according to the invention show a reversible binding to the immobilized metal ions which is at least 1.5 times stronger, preferably at least twice, and particularly preferably at least three times, stronger. Advantageous sequences make it possible for the protein yield after the purification to be at least 20%, preferably at least 30%, particularly preferably at least 40%, very particularly preferably at least 50%.

E1

Amend Table I on page 19, lines 20-38, as follows:

E2

Clone	Amino acid sequence											
A6	His	Gln	His	Glu	Gly	Arg	Cys	Lys	Glu	Cys	gfp	SEQ ID NO:2
A8	His	Cys	His	Pro	Glu	Leu	Cys	Stop	Leu	Cys	gfp	SEQ ID NO:1
A13	His	Leu	His	Ser	Ile	Gly	Cys	Pro	Stop	Cys	gfp	SEQ ID NO:1
M13	His	Asn	His	Arg	Tyr	Gly	Cys	Gly	Cys	Cys	gfp	SEQ ID NO:3
M14	His	Ser	His	Ser	Val	Gly	Cys	Phe	Phe	Cys	gfp	SEQ ID NO:1
M15	His	Gly	His	Thr	Leu	Ser	Cys	Gly	Leu	Cys	gfp	SEQ ID NO:1
M16	His	Ser	His	Thr	Leu	Arg	Cys	Lys	Gly	Cys	gfp	SEQ ID NO:1
M16a	His	Ser	His	Stop	Leu	Arg	Cys	Lys	Gly	Cys	gfp	SEQ ID NO:1
Z4	His	Stop	His	Asn	Stop	Val	Cys	Ala	Thr	Cys	gfp	SEQ ID NO:1
Z5	His	Arg	His	Gly	Thr	Asn	Cys	Leu	Lys	Cys	gfp	SEQ ID NO:4
Z7	His	Ile	His	Gln	Ser	Asn	Cys	Gln	Val	Cys	gfp	SEQ ID NO:5
Z11	His	Thr	His	Ala	Ser	Gly	Cys	Stop	Stop	Cys	gfp	SEQ ID NO:1
Z13	His	Cys	His	Thr	Trp	Cys	Cys	Asn	Stop	Cys	gfp	SEQ ID NO:1

Amend Table II on page 20, lines 1-24, as follows:

Clone	Amino acid sequence											
A1	His	Gly	His	Met	Glu	Arg	Cys	Leu	Val	Cys	gfp	SEQ ID NO:1
A2	His	Lys	His	Ala	Arg	Ser	Cys	Met	Gly	Cys	gfp	SEQ ID NO:1
A3	His	Phe	His	Thr	Val	Phe	Cys	Phe	Ser	Cys	gfp	SEQ ID NO:1
A4	His	Arg	His	Arg	Gly	Met	Cys	Thr	Ala	Cys	gfp	SEQ ID NO:1
A12	His	Asp	His	Arg	Gly	Val	Cys	Gly	Leu	Cys	gfp	SEQ ID NO:1
A14	His	Asp	His	Glu	Arg	Leu	Cys	His	Asn	Cys	gfp	SEQ ID NO:1
X8	His	Gly	His	Gly	Asn	Arg	Cys	Cys	Gly	Cys	gfp	SEQ ID NO:1
X9	His	Arg	His	Gly	Thr	Ala	Cys	Met	Asp	Cys	gfp	SEQ ID NO:1
X11	His	Ile	His	Ile	Met	Thr	Cys	Leu	Ser	Cys	gfp	SEQ ID NO:1
X12	His	Thr	His	Pro	Arg	Ser	Cys	Ala	Glu	Cys	gfp	SEQ ID NO:1
X15	His	Gly	His	Asp	Arg	Thr	Cys	Arg	Gly	Cys	gfp	SEQ ID NO:1
X16	His	Arg	His	Ala	Ile	Ser	Cys	Ile	Gly	Cys	gfp	SEQ ID NO:1
X17	His	Ile	His	Arg	Gly	Asp	Cys	Tyr	Glu	Cys	gfp	SEQ ID NO:1
X18	His	His	His	Gly	Ser	Thr	Cys	Pro	Thr	Cys	gfp	SEQ ID NO:1
X19	His	His	His	Phe	His	Ser	Cys	Phe	Tyr	Cys	gfp	SEQ ID NO:1
Z8	His	Lys	His	Val	Asp	His	Cys	Gly	Arg	Cys	gfp	SEQ ID NO:1
Z9	His	Ser	His	Leu	Thr	Leu	Cys	Leu	Gly	Cys	gfp	SEQ ID NO:1
Z10	His	Thr	His	Gln	Ser	Gln	Cys	Gly	Arg	Cys	gfp	SEQ ID NO:1
Z14	His	Arg	His	Leu	Phe	Trp	Cys	Ser	Glu	Cys	gfp	SEQ ID NO:1

E3

IN THE CLAIMS

Amend claims 1, 6 and 15 as follows:

1.(currently amended) A peptide fragment having the general sequence

His-X^1-His-X^2-X^3-X^4-Cys-X^5-X^6-Cys (SEQ ID NO:1),

where the variables X^1 to X^6 in the sequence have the following meanings:

E4

X^1 = an amino acid selected from the group consisting of Ala, Val, Phe, Ser, Met, Trp, Tyr, Asn, Asp or Lys and the variables X^2 to X^6 an amino acid selected from the group consisting of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His or

X^2 = an amino acid selected from the group consisting of Val, Ile, Phe, Pro, Trp,

Tyr, Gln, Glu or Arg and the variables X^1, X^3 to X^6 an amino acid selected from the group consisting of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His or

X^3 = an amino acid selected from the group consisting of Gly, Ile, Thr, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His and the variables X^1, X^2, X^4 to X^6 an amino acid selected from the group consisting of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His or

EH cont

X^4 = an amino acid selected from the group consisting of Val, Phe, Pro, Cys, Met, Trp, Asn, Glu, Arg or His and the variables X^1 to X^3, X^5, X^6 an amino acid selected from the group consisting of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His or

X^5 = an amino acid selected from the group consisting of Gly, Ser, Cys, Met, Trp, Asn, Glu, Lys or Arg and the variables X^1 to X^4, X^6 an amino acid selected from the group consisting of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His or

X^6 = an amino acid selected from the group consisting of Phe, Pro, Ser, Cys, Trp, Tyr or Gln and the variables X^1 to X^5 an amino acid selected from the group consisting of Gly, Ala, Val, Leu, Ile, Phe, Pro, Ser, Thr, Cys, Met, Trp, Tyr, Asn, Gln, Asp, Glu, Lys, Arg, His and

where at least one of the variables X^1 to X^6 in the sequence is, independently of one another, Gln or Asn.

6. (currently amended) A peptide fragment having the sequence

His-Gln-His-Glu-Gly-Arg-Cys-Lys-Glu-Cys (SEQ ID NO:2)

His-Asn-His-Arg-Tyr-Gly-Cys-Gly-Cys-Cys (SEQ ID NO:3)

E5

His-Arg-His-Gly-Thr-Asn-Cys-Leu-Lys-Cys (SEQ ID NO:4)

His-Ile-His-Gln-Ser-Asn-Cys-Gln-Val-Cys (SEQ ID NO:5).

15. (currently amended) A process for preparing protein fragments able to enter into a reversible affinity linkage with immobilized metal ions, which comprises carrying out the following steps:

a) preparing a nucleic acid library starting from any suitable nucleic acid sequence which codes for a protein fragment of the sequence

E6

His-X^1-His-X^2-X^3-X^4-Cys-X^5-X^6-Cys (SEQ ID NO:11),

where the histidine and cysteine residues of the sequence are conserved in the nucleic acid library,

b) fusing the nucleic acids of the library to a reporter gene which makes it possible to detect the fusion protein encoded by the resulting nucleic acid via its binding to the immobilized metal ions and

c) selecting the nucleic acid sequences which display a reversible binding to the immobilized metal ions which is at least 1.5 times stronger than the sequence in the natural Helicobacter pylori ATPase-439.